

SEQUENCE LISTING

<110> Pharmacia AB

<120> Protein Cluster II

<130> 00404

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<170> PatentIn version 3.0

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<212> DNA

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<221> CDS

<222> (21)..(497)

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<222> (297)..()

<223> n=a, g, c or t

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	1				5					10		
aaa tcc tgg ctg aat ttt tta acc ttc ctc tat gga tcg gca ata ggg	101											
Lys Ser Trp Leu Asn Phe Leu Thr Phe Leu Tyr Gly Ser Ala Ile Gly												
	15	20	25									
ttt att tta ttt tct cag cta ctt agt att ttg ttg gga gaa gag ggt	149											
Phe Ile Leu Phe Ser Gln Leu Leu Ser Ile Leu Leu Gly Glu Glu Gly												
	30	35	40									
gac acc cag act aat gtt ctt cat aat gat cct cat gcg agg cat tca	197											
Asp Thr Gln Thr Asn Val Leu His Asn Asp Pro His Ala Arg His Ser												
	45	50	55									
gat gat aat gga cag aat cat cta gga gga caa atg aac ttc aat gca	245											
Asp Asp Asn Gly Gln Asn His Leu Gly Gly Gln Met Asn Phe Asn Ala												
	60	65	70	75								
gat tct agc caa cgt aaa gat gag aac aca gaa atc gct gaa aac ctc	293											
Asp Ser Ser Gln Arg Lys Asp Glu Asn Thr Glu Ile Ala Glu Asn Leu												
	80	85	90									
tat nag caa gtt aaa att ctt tgc tgg gtt atg aca ggc tct caa aac	341											
Tyr Xaa Gln Val Lys Ile Leu Cys Trp Val Met Thr Gly Ser Gln Asn												
	95	100	105									
cta cag aaa aag gcc aaa cat gtc aaa gct aca tgg gcc cag cgt tgt	389											
Leu Gln Lys Lys Ala Lys His Val Lys Ala Thr Trp Ala Gln Arg Cys												
	110	115	120									
cta aaa gta ttt ttt atg agt tca gaa gaa aat aaa gac ttc cgt gct	437											
Leu Lys Val Phe Phe Met Ser Ser Glu Glu Asn Lys Asp Phe Arg Ala												
	125	130	135									
gtg gga ttg aaa acc aaa gca ggc aga gat gag cta tac tgg aaa aca	485											
Val Gly Leu Lys Thr Lys Ala Gly Arg Asp Glu Leu Tyr Trp Lys Thr												
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att aac ctt ttc agtatggt	505											
Ile Asn Leu Phe												

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Gln Leu Leu Ser Ile Leu Leu Gly Glu Glu Gly Asp Thr Gln Thr Asn
35 40 45

Val Leu His Asn Asp Pro His Ala Arg His Ser Asp Asp Asn Gly Gln
50 55 60

Asn His Leu Gly Gly Gln Met Asn Phe Asn Ala Asp Ser Ser Gln Arg
65 70 75 80

Lys Asp Glu Asn Thr Glu Ile Ala Glu Asn Leu Tyr Xaa Gln Val Lys
85 90 95

Ile Leu Cys Trp Val Met Thr Gly Ser Gln Asn Leu Gln Lys Lys Ala
100 105 110

Lys His Val Lys Ala Thr Trp Ala Gln Arg Cys Leu Lys Val Phe Phe
115 120 125

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Lys Ala Gly Arg Asp Glu Leu Tyr Trp Lys Thr Ile Asn Leu Phe
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Tyr Asn Pro Asp Glu Ser Thr Tyr Phe Gly Lys Arg Phe Lys His Cys
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tct agc caa cat aaa gat gag aac aca gac att gct gaa aac ctc tat 97
Ser Ser Gln His Lys Asp Glu Asn Thr Asp Ile Ala Glu Asn Leu Tyr
20 25 30
cag aaa gtt aga att ctt tgc tgg gtt atg acc ggc cct caa aac cta 145
Gln Lys Val Arg Ile Leu Cys Trp Val Met Thr Gly Pro Gln Asn Leu
35 40 45
gag aaa aag gcc aaa cac gtc aaa gct act tgg gcc cag cgt tgt aac 193
Glu Lys Lys Ala Lys His Val Lys Ala Thr Trp Ala Gln Arg Cys Asn
50 55 60
aaa gtg ttg ttt atg agt tca gaa gaa aat aaa gac ttc cct gct gtg 241
Lys Val Leu Phe Met Ser Ser Glu Glu Asn Lys Asp Phe Pro Ala Val
65 70 75 80
gga ctg aaa acc aaa gaa ggc aga gat caa cta tac tgg aaa aca att 289
Gly Leu Lys Thr Lys Glu Gly Arg Asp Gln Leu Tyr Trp Lys Thr Ile
85 90 95
aaa gct ttt cag tat gtt cat gaa cat tat tta caa gat gct gat tgg 337
Lys Ala Phe Gln Tyr Val His Glu His Tyr Leu Gln Asp Ala Asp Trp
100 105 110
ttt ttg aaa gca gat gat gac acg tat gtc ata cta gac aat ttg agg 385
Phe Leu Lys Ala Asp Asp Asp Thr Tyr Val Ile Leu Asp Asn Leu Arg
115 120 125
tgg ctt ctt tca aaa tac gac cct gaa gaa ccc att tac ttt ggg aga 433
Trp Leu Leu Ser Lys Tyr Asp Pro Glu Glu Pro Ile Tyr Phe Gly Arg
130 135 140
aga ttt aag cct tat gta aag cag ggc tac atg agt gga gga gca gga 481
Arg Phe Lys Pro Tyr Val Lys Gln Gly Tyr Met Ser Gly Gly Ala Gly
145 150 155 160
tat gta cta agc aaa gaa gcc ttg aaa aga ttt gtt gat gca ttt aaa 529
Tyr Val Leu Ser Lys Glu Ala Leu Lys Arg Phe Val Asp Ala Phe Lys
165 170 175
aca gac aag tgt aca cat agt tcc tcc att gaa gac tta gca ctg ggg 577
Thr Asp Lys Cys Thr His Ser Ser Ile Glu Asp Leu Ala Leu Gly
180 185 190

aga tgc atg gaa att atg aat gta gaa gca gga gat tcc aga gat acc 625
 Arg Cys Met Glu Ile Met Asn Val Glu Ala Gly Asp Ser Arg Asp Thr
 195 200 205

att gga aaa gaa act ttt cat ccc ttt gtg cca gaa cac cat tta att 673
 Ile Gly Lys Glu Thr Phe His Pro Phe Val Pro Glu His His Leu Ile
 210 215 220

aaa ggt tat cta cct aga acg ttt tgg tac tgg aat tac aac tat tat 721
 Lys Gly Tyr Leu Pro Arg Thr Phe Trp Tyr Trp Asn Tyr Asn Tyr Tyr
 225 230 235 240

cct cct gta gag ggt cct ggt tgc tgc tct gat ctt gca gtt tct ttt 769
 Pro Pro Val Glu Gly Pro Gly Cys Cys Ser Asp Leu Ala Val Ser Phe
 245 250 255

cac tat gtt gat tct aca acc atg tat gag tta gaa tac ctc gtt tat 817
 His Tyr Val Asp Ser Thr Thr Met Tyr Glu Leu Glu Tyr Leu Val Tyr
 260 265 270

cat ctt cgt cca tat ggt tat tta tac aga tat caa cct acc tta cct 865
 His Leu Arg Pro Tyr Gly Tyr Leu Tyr Arg Tyr Gln Pro Thr Leu Pro
 275 280 285

gaa cgt ata cta aag gaa att agt caa gca aac aaa aat gaa gat aca 913
 Glu Arg Ile Leu Lys Glu Ile Ser Gln Ala Asn Lys Asn Glu Asp Thr
 290 295 300

aaa gtg aag tta gga aat cct tgaaagaaaa tcatgaatga acaaaggtaa 964
 Lys Val Lys Leu Gly Asn Pro
 305 310

tatgtctagc actgcactga aaaaggactt ctgcatttct gacatagaac actggaatcc 1024

cagtgaggaa ttctaagtga acattcctta tagaaacctt tcacatgaat gactataaac 1084

tgaagcttta aatgagctgt gaagtgtggt aaaatgtggt ttgatacagt aatatataaa 1144

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Gln Lys Val Arg Ile Leu Cys Trp Val Met Thr Gly Pro Gln Asn Leu
 35 40 45

Glu Lys Lys Ala Lys His Val Lys Ala Thr Trp Ala Gln Arg Cys Asn
50 55 60

Lys Val Leu Phe Met Ser Ser Glu Glu Asn Lys Asp Phe Pro Ala Val
65 70 75 80

Gly Leu Lys Thr Lys Glu Gly Arg Asp Gln Leu Tyr Trp Lys Thr Ile
85 90 95

Lys Ala Phe Gln Tyr Val His Glu His Tyr Leu Gln Asp Ala Asp Trp
100 105 110

Phe Leu Lys Ala Asp Asp Asp Thr Tyr Val Ile Leu Asp Asn Leu Arg
115 120 125

Trp Leu Leu Ser Lys Tyr Asp Pro Glu Glu Pro Ile Tyr Phe Gly Arg
130 135 140

Arg Phe Lys Pro Tyr Val Lys Gln Gly Tyr Met Ser Gly Gly Ala Gly
145 150 155 160

Tyr Val Leu Ser Lys Glu Ala Leu Lys Arg Phe Val Asp Ala Phe Lys
165 170 175

Thr Asp Lys Cys Thr His Ser Ser Ser Ile Glu Asp Leu Ala Leu Gly
180 185 190

Arg Cys Met Glu Ile Met Asn Val Glu Ala Gly Asp Ser Arg Asp Thr
195 200 205

Ile Gly Lys Glu Thr Phe His Pro Phe Val Pro Glu His His Leu Ile
210 215 220

Lys Gly Tyr Leu Pro Arg Thr Phe Trp Tyr Trp Asn Tyr Asn Tyr Tyr
225 230 235 240

Pro Pro Val Glu Gly Pro Gly Cys Cys Ser Asp Leu Ala Val Ser Phe
245 250 255

His Tyr Val Asp Ser Thr Thr Met Tyr Glu Leu Glu Tyr Leu Val Tyr
260 265 270

His Leu Arg Pro Tyr Gly Tyr Leu Tyr Arg Tyr Gln Pro Thr Leu Pro
275 280 285

Glu Arg Ile Leu Lys Glu Ile Ser Gln Ala Asn Lys Asn Glu Asp Thr
290 295 300

Lys Val Lys Leu Gly Asn Pro
305 310